

RESPONSE TO RESTRICTION REQUIREMENT
U.S. Appln. No. 10/533,166 (Q87648)

REMARKS

On page 2 of the Office Action, the Examiner issues a Restriction Requirement under 35 U.S.C. § 121 to one of the inventions of the following groups:

- Group I - Claims 1-6, drawn to a PCR method;
- Group II - Claims 7-17, drawn to primers and kits;
- Group III - Claim 18, drawn to a method of extracting nucleic acid from soil;
- Group IV - Claim 19, drawn to a kit for extracting nucleic acid from soil;
- Group V - Claim 20, drawn to a method of extracting pathogen DNA from host vegetable tissue;
or
- Group VI - Claim 21, drawn to a kit for extracting pathogen DNA from host vegetable tissue.

Specifically, the Examiner contends that restriction is proper because the inventions of Groups I-VI do not relate to a single inventive concept, i.e., Matsumoto et al teaches SEQ ID NO:1 of Group II.

Accordingly, Applicant hereby elect the invention of Group II, i.e., primer Claims 7-17 (now Claims 7, 10-14 and 17, and new Claim 22) without traverse. However, Applicants request rejoinder of method Claims 1-6 (now Claims 1, 4 and 6) upon allowance of the elected invention.

Claims 18-21 are hereby cancelled without prejudice to pursue the same in a Divisional Application(s).

In any event, the Examiner is requested to note that Matsumoto et al does not teach a primer of SEQ ID NO:1

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(formula Ia). Specifically, the EMBL database entry for the sequence of Matsumoto sequence (a copy of which is attached hereto), shows that the sequence of Matsumoto et al is 774 nucleotides (nts) in length. While the sequence of formula Ia may fall within these 774 nts, Matsumoto et al does not specifically teach the 21 nt sequence of formula Ia (alone), nor does Matsumoto et al render obvious the 21 nt sequence of formula Ia, which has in any event been cancelled from the elected Claims. Thus, contrary to the Examiner's contention "the product (primer SEQ ID NO: 1) of group II was "not" known to one of ordinary skill in the art at the time of the invention".

Furthermore, the Claims are all limited to primers which are 18 to 24mers (cf. the sequence of Matsumoto et al is 774 nts in length). Hence, the scope of these claims cannot be said to encompass the sequence of Matsumoto et al.

In addition, on page 3 of the Office Action, the Examiner issues an Election of Species Requirement, i.e., to a specific species of pathogens amongst:

- i. *M. acerina*,
- ii. *F. carotae*, and
- iii. *Pythium* species.

Accordingly, Applicant hereby elect species iii, i.e., *Pythium* species without traverse.

The Examiner is requested to note that the primers of formula Ia-Xb fall within this species, whereas the primers of formula XIa-XIVb do not.

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Thus, Applicants hereby amend the claims such that they are limited to the elected species, without prejudice to the filing of a Divisional Application(s) thereon.

In addition, on page 4 of the Office Action, the Examiner issues a Restriction Requirement, i.e., a specific SEQ ID NO primer pair.

Accordingly, Applicant hereby elect the primer pair, IXa-IXb (SEQ ID Nos 17-18) with traverse.

As noted by the Examiner, upon allowance of the elected species, Applicants will be entitled to consideration of additional species.

More specifically, primers having the sequences of IXa-IXb can be used for the detection of *P. sylvaticum* (see Examples 1-10 and 19, particularly Table 1).

However, the Examiner is requested to note that the Claims refer to primers which:

"**hybridize** to an oligonucleotide sequence selected from the group consisting of formulae Ib ..., IIB ...[etc.]".

Hence, the claims are actually referring to primers which are **complementary** to the specified primers. Primers which are complementary to the oligonucleotides of formulae IXa and IXb are given in formulae IVa and IVb, respectively.

The Examiner is requested to note that other pairs of primers are complementary in this same way, e.g., primers VIIa and VIIb with primers IIa and IIB, primers VIIIA and VIIIB with primers IIIa and IIIB, and primers Xa and Xb with primers Va and Vb.

In view of the relationship between primers IXa/IXb and IVa/IVb (i.e., the latter pair are complementary to the

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former pair), all 4 primers relate to the same invention. Thus, primers IVa/IVb also relate to the same invention as primers IXa/IXb. Further, the primers of Group B, in the attachment hereto are unified by virtue of their binding to a small region of DNA within the rRNA gene, the DNA sequence of which is not conserved between *Pythium* species (i.e., priming in this region can lead to species-specific amplification by PCR) but which falls between two highly-conserved regions (the regions in which generic primers G2 and G4 bind, respectively). Furthermore, each primer set is specific to a *Pythium* sub-species that is a root vegetable pathogen, e.g. responsible for cavity spot in carrots.

The primers of Group A in the attachment hereto, directed to a different region of DNA within the rRNA gene, are hereby cancelled from the elected Claims without prejudice to pursue the same in a Divisional Application.

The Examiner is requested to note that the method of Claim 1 does not require both primers to be species-specific in order to work, i.e., only one primer need be species specific.

The Examiner is requested to note that Wang et al, "Development of a Species-Specific Primer for *Pythium violae*", British Crop Protection Council Symposium Proceedings, 65:205-210 (1996) (a copy of which is attached to the Information Disclosure Statement filed simultaneously herewith), discloses a PCR primer (Pv1) (Figure 1, page 209, see the underlined sequence) which is an 19mer oligo. This sequence may overlap with the sequence of formula VIIa, the complementary sequence to primer IIa. The 19mer is said to have been used as

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a *Pythium violae*-specific PCR primer. However, primers VIIa and IIa have been deleted from the elected claims.

The Examiner is invited to contact the undersigned at the below listed number on any questions which might arise.

Respectfully submitted,

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WASHINGTON OFFICE

23373

CUSTOMER NUMBER

Date: December 6, 2007


Gordon Kit

Registration No. 30,764

ANNEX 1

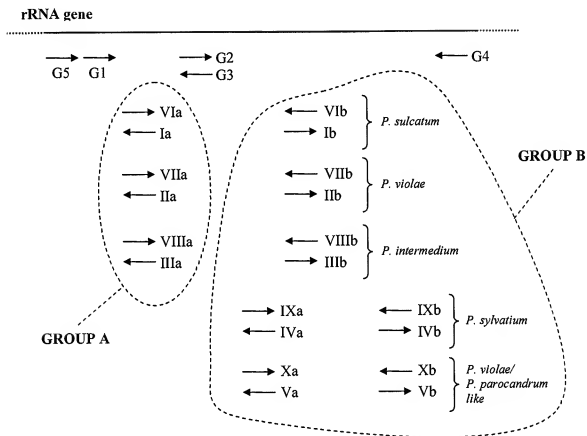


Diagram showing the relative positions and orientations of primers Ia to Xb within the rRNA genes of different *Pythium* species. (Primers G1 to G5 represent non-claimed, generic (i.e. any fungi) rDNA primers that may be used with the primers of the invention)

Search CoreNucleotide for [] [Go] [Clear]

Limits Preview/Index History Clipboard Details

Display GenBank Show 5 Send to Hide: ☐ sequence ☐ all but gene, CDS and mR

Range: from begin to end ☐ Reverse complemented strand Features: [] [Refresh]

[1: AJ233458] Reports Pythium sulcatum ...[gi:6468685] Links

Features Sequence

LOCUS AJ233458 774 bp DNA linear PLN 24-NOV-1999
 DEFINITION Pythium sulcatum ITS1, 5.8S rRNA gene and ITS2, strain CTMa7.
 ACCESSION AJ233458
 VERSION AJ233458.1 GI:6468685
 KEYWORDS 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer;
 ITS1; ITS2.

SOURCE Pythium sulcatum
 ORGANISM Pythium sulcatum
 Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 Pythium.

REFERENCE 1
 AUTHORS Matsumoto, C., Kageyama, K., Suga, H. and Hyakumachi, M.
 TITLE Phylogenetic relationships of Pythium species based on ITS and 5.8S
 sequences of the ribosomal DNA
 JOURNAL Mycoscience 40, 321-331 (1999)
 REFERENCE 2 (bases 1 to 774)

AUTHORS Kageyama, K.
 TITLE Direct Submission
 JOURNAL Submitted (22-SEP-1998) Kageyama K., Gifu university, Yanagido,
 1-1, Gifu 501-1193, Japan

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 /gene="5.8S rRNA"
 rRNA 172..330
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 /product="5.8S ribosomal RNA"
 misc_feature 331..774
 /note="internal transcribed spacer 2 (ITS2)"

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721 acaacaccaa ttggtggacag ttgtgggat ttatctgca ggcgcttttt tcaa

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